INFORMATION DISCLOSURE STATEMENT	Atty. Docket No.: 00032.US1	Serial No.: 09/825,212
	Applicant(s): Timothy E. Benson	Confirmation No.: 2707
	Filing Date: April 3, 2001	Group: 1645

U.S. PATENT DOCUMENTS

Examiner Initial		Document Number	Date	Name	Class	Subclass	Filing Date If Appropriate
		none					

FOREIGN PATENT DOCUMENTS

Examiner Initial		Document Number	Date	Country	Class	Subclass	Translation	
							Yes	No
ME		WO 99/45123	09/10/99	PCT				

OTHER DOCUMENTS (Including Authors, Title, Date, Pertinent Papers, etc.)

Examiner Initial		Document Description
ME		Bellizzi et al., "Producing selenomethionine-labeled proteins with a baculovirus expression vector system," *Structure Fold Des.* 1999 Nov 15;7(11):R263-7.
ME		Greer, "Protein structure and function by comparative model building," *Ann N Y Acad Sci.* 1985;*439*:44-63.
ME		Greer, "Comparative modeling methods: application to the family of the mammalian serine proteases," *Proteins.* 1990;*7*(4):317-34.
ME		Jancarik et al., "Sparse matrix sampling: a screening method for crystallization of proteins," *J Appl Cryst.*, 1991; *24*:409-411.
ME		Kuntz et al., "Structure-based molecular design," *Accounts Chemical Res.* 1994 May; *27*(5):117-123.

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Examiner Initial		Document Number	Date	Country	Class	Subclass	Translation Yes	Translation No
NC		EP 786 519 A2	07/30/97	Europe				
NC		WO 99/47639 A2	09/23/99	PCT				
NC		WO 99/47662 A1	09/23/99	PCT				
NC		WO 00/12678 A2	03/09/00	PCT				
NC		WO 00/12678 A3	03/09/00	PCT				
NC		WO 01/16292 A2	03/08/01	PCT				

OTHER DOCUMENTS (Including Authors, Title, Date, Pertinent Papers, etc.)

Examiner Initial		Document Description
NC		Åslund et al., "The thioredoxin superfamily: redundancy, specificity, and gray-area genomics," *J Bacteriol.* 1999 Mar;*181*(5):1375-9.
NC		Bartlett et al., "CAVEAT: A program to facilitate the structure-derived design of biologically active molecules," *Molecular Recognition: Chemical and Biological Problems*, Royal Society of Chemistry, Special Pub No. 78:182-196 (1989).
NC		Benson et al., "An enzyme-substrate complex involved in bacterial cell wall biosynthesis," *Nat Struct Biol.* 1995 Aug;*2*(8):644-53.
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NC		Brünger, "X-PLOR: Version 3.1, a System for X-Ray Crystallography and NMR", Yale University Press, New Haven & London, 1992; cover page, publication page and table of contents: 13 pages.
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NE		Cowtan et al., "Improvement of Macromolecular Electron-Density Maps by the Simultaneous Application of Real and Reciprocal Space Constraints," *Acta Crystallogr D Biol Crystallogr.* 1993 Jan 1;*49*(1):148-157.
NE		Cowtan et al., "Miscellaneous algorithms for density modification," *Acta Crystallogr D Biol Crystallogr.* 1998 Jul 1;*54*(4):487-93.
NE		Dai et al., "Crystal structure of *Arabidopsis thaliana* NADPH dependent thioredoxin reductase at 2.5 Å resolution," *J Mol Biol.* 1996 Dec 20;*264*(5):1044-57.
NE		delCardayre et al., "Coenzyme A disulfide reductase, the primary low molecular weight disulfide reductase from *Staphylococcus aureus*. Purification and characterization of the native enzyme," *J Biol Chem.* 1998 Mar *6*;273(10):5744-51.
NE		Eisen et al., "HOOK: a program for finding novel molecular architectures that satisfy the chemical and steric requirements of a macromolecule binding site," *Proteins: Struct. Funct. Genet.* 1994 Jul;*19*(3):199-221.
NE		Evans, "SETOR: hardware-lighted three-dimensional solid model representations of macromolecules," *J Mol Graph.* 1993 Jun;*11*(2):134-8.
NE		Finzel, "LORE: exploiting database of known structures," *Meth. Enzymol.* 1997; *277*(B):230-42.
NE		Gillet et al., "SPROUT: a program for structure generation," *J Comput Aided Mol Des.* 1993 Apr;*7*(2):127-53.
NE		Goodford, "A computational procedure for determining energetically favorable binding sites on biologically important macromolecules," *J Med Chem.* 1985 Jul; *28*(7):849-57.
NE		Goodsell et al., "Automated docking of substrates to proteins by simulated annealing," *Proteins: Struct. Funct. Genet.* 1990;*8*(3):195-202.
NE		Hendrickson, "Determination of macromolecular structures from anomalous diffraction of synchrotron radiation," *Science.* 1991 Oct 4;*254*(5028):51-8.
NE		Jiang et al., "Protein hydration observed by X-ray diffraction. Solvation properties of penicillopepsin and neuraminidase crystal structures," *J Mol Biol.* 1994 Oct 14;*243*(1):100-15.
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Examiner Initial*	Document Description
	Kuntz et al., "A geometric approach to macromolecule-ligand interactions," *J Mol Biol.* 1982 Oct 25;*161*(2):269-88.
	Kuriyan et al., "Crystallization and preliminary x-ray characterization of thioredoxin reductase from *Escherichia coli*," *J Biol Chem.* 1989 Aug 5;*264*(22):12752-3.
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NE		Otwinowski, "Maximum likelihood refinement of Heavy atom parameters," *Isomorphous replacement and anomalous scattering - Proceedings of the CCP4 Study Weekend 25-26 January 1991*, (W. Wolf et al., eds.) Science and Engineering Research Counsel, Daresbury Laboratory, Warrington, U.K. (1991) pp. 80-86.
NE		Ramakrishnan et al., "Crystal structure of globular domain of histone H5 and its implications for nucleosome binding," *Nature*. 1993 Mar 18;*362*(6417):219-23.
NE		Rossmann, ed., *The Molecular Replacement Method - A Collection of Papers on the Use of Non-Crystallographic Symmetry, Intl. Sci. Rev. Ser. No. 13*, Gordon & Breach, New York, NY; title page, publication page, and table of contents only, 6 pages (1972).
NE		Sack, "CHAIN - A Crystallographic Modeling Program," *J Molecular Graphics*. 1988 Dec; *6*(4):224-5.
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